

CURRICULUM VITAE

10/29/2014

Julia Krushkal, PhD

Current position: Research Computational Biologist
Biometric Research Branch
National Cancer Institute, National Institutes of Health
9609 Medical Center Drive, Room 5W116, Rockville, MD 20850
Tel. 240-276-5988, email julia.krushkal@nih.gov

Research Interests: Bioinformatic analysis of genome sequence, expression, and epigenetic data, statistical genetics, genetic epidemiology

Education and Training

Ph.D. **Genetics**, 1996. Ph.D. advisor: Dr. Wen-Hsiung Li.
The University of Texas Health Science Center at Houston

Honors Diploma **Cytology and genetics with concentration in mathematical biology**, 1990
(equivalent of B.S./M.S. with distinction) Novosibirsk State University (Russia)

Additional Training: 1993-1994: **Courses in statistics and computer programming**, Rice University
2006-2009: **Courses in statistics and programming**
The University of Tennessee Health Science Center
2012: **Scientific Review Officer training** in review and extramural funding procedures at the National Institutes of Health

Professional Experience

10.2014-present Research Computational Biologist, Biometric Research Branch
National Cancer Institute, National Institutes of Health, Rockville, MD

01.2012-10.2014 Scientific Review Officer, Population Sciences and Epidemiology IRG
Division of AIDS, Behavioral, and Population Sciences, Center for Scientific Review
National Institutes of Health, Bethesda, MD

07.2010-01.2012 Associate professor (*with tenure*), Department of Preventive Medicine,
The University of Tennessee Health Science Center, Memphis, TN

09.2007-06.2010 Assistant professor (*tenure track*), Department of Preventive Medicine
The University of Tennessee Health Science Center

07.2007-01.2012 Faculty affiliate member, Program in Bioinformatics, The University of Memphis

09.2002 - 08.2007 Assistant Professor (*non-tenure track*)
Department of Preventive Medicine and Center of Genomics and Bioinformatics
The University of Tennessee Health Science Center

07.2007 Research visitor: Collaborative research in bioinformatics. The University of Sydney.

01.2000 – 05.2002 Visiting Assistant Professor, Department of Biology and Biotechnology
Worcester Polytechnic Institute, Worcester, MA

05.1997 – 12.1999 Assistant Professor (*non-tenure track/research*)
Institute of Molecular Medicine for the Prevention of Human Disease,
The University of Texas Health Science Center at Houston

06.1996 – 04.1997 Postdoctoral Fellow. Laboratory of Dr. Eric Boerwinkle.
Human Genetics Center, The University of Texas Health Science Center at Houston

08.1991 – 05.1996 Graduate Student (Graduate Research Assistant).
Graduate School of Biomedical Sciences, Program in Genetics,
The University of Texas Health Science Center at Houston

08.1990 – 08.1991 Research Trainee, Theoretical Department, Institute of Cytology and Genetics,
Siberian Branch of the USSR Academy of Sciences, Novosibirsk, Russia

Past Grants, Fellowships, and Awards

- 06/10/11-01/18/12 NIH/NICHD HD-060713 R01 *Genomics and epigenomics of fetal growth regulation*. \$1,289,404 (**J. Krushkal, PI**) **Principal Investigator**
- 06/10/11-08/31/12 NIH/NICHD HD-055462 R01 *Maternal-fetal conflict: The effect of imprinted genes on fetal growth*. \$723,663 (**J. Krushkal, PI**) **Principal Investigator**.
- 10/01/10-08/31/12 NIH/NHLBI *Women's Health Initiative 2010-2015 extension study*. \$303,339 (Subcontract with Wake Forest University Health Sciences; K. Johnson, site PI) Co-Investigator.
- 08/15/05-08/31/11 DOE DE-FC02-02ER63446 *Genome-based models to optimize in situ bioremediation of uranium and harvesting electrical energy from waste organic matter* (D. Lovley, project PI; **J. Krushkal, UT-Memphis site PI**). **Principal Investigator of the subcontract** with the University of Massachusetts. \$652,519- University of Tennessee subcontract only.
- 0/01/09-06/30/11 UTHSC Clinical and Translational Science Institute *Molecular predictors of statin intolerance in patients with dyslipidemia*. \$99,289 (M. B. Elam, PI) Co-investigator
- 10/01/09-06/30/11 UTHSC Clinical and Translational Science Institute *Quantitative gene expression using a novel technology to predict chemosensitivity of breast cancer*. \$90,809 (J. Sachdev, PI) Co-investigator
- 08/01/09-06/09/11 NIH/NICHD HD-060713 R01 *Genomics and epigenomics of fetal growth regulation*. \$1,289,404 (R. Adkins, PI) Co-investigator
- 09/01/11-06/09/11 NIH/NICHD HD-055462 R01 *Maternal-fetal conflict: The effect of imprinted genes on fetal growth*. \$723,663 (R. Adkins, PI) Co-investigator
- 08/01/08-06/30/10 University of Tennessee Clinical and Translational Science Institute. *Genomics and epigenomics of fetal growth regulation and cognitive development*. (R. Adkins, PI) \$79,998. Co-Investigator
- 11/01/07-08/31/09 NIH/NLM R13 LM009315 *Annual UT-ORNL-KBRIN Bioinformatics Summit* (E. Rouchka, PI; **J. Krushkal, UT-Memphis site PI**). **Principal Investigator of the subcontract** with the University of Louisville. \$6,331 - University of Tennessee subcontract only
- 09/01/07-08/31/09 NIH/ NICHD R01 HD-055462-01 *Maternal-fetal conflict: The effect of imprinted genes on fetal growth*. (R. Adkins, PI). \$372,300. Co-Investigator
- 07/01/03-06/31/08 NIH/NHLBI R01 HL072375 *Genetics of cardiovascular reactivity in black youth* (B. Alpert, PI). \$2,376,320. Consultant
- 10/01/06-07/31/07 *Genetic polymorphisms in pediatric lung injury*. Contract work in genetic epidemiology for the Medical College of Wisconsin, \$6,000.
- 07/01/04-09/30/06 NIH/NICHD R21 HD4767 *Genetic polymorphisms in pediatric lung injury* (M. Quasney, PI). \$401,500. Collaborator.
- 09/01/02-08/31/05 DOE DE-FC02-02ER63446 *Analysis of the genetic potential and gene expression of microbial communities involved in the in situ bioremediation of uranium and harvesting electrical energy from organic matter* (D. Lovley, PI; **J. Krushkal, UT-Memphis site PI**). **Principal Investigator of the subcontract** with University of Massachusetts, \$196,460- University of Tennessee subcontract only.
- 01/01/05-12/31/05 Children's Foundation Research Center, Le Bonheur Children's Hospital. *Molecular genetic analysis of birth weight variation* (R. Adkins, PI) \$50,000. Investigator.
- 01/01/04-12/31/04 Children's Foundation Research Center, Le Bonheur Children's Hospital, Memphis, TN *Molecular genetic analysis of birth weight variation* (R. Adkins, PI). \$50,000. Investigator.

01/01/03-12/31/03	Children's Foundation Research Center, Le Bonheur Children's Hospital, Memphis, TN. <i>Molecular Genetic Analysis of Pre-Eclampsia</i> (R. Adkins, PI). \$74,000. <u>Consultant</u> .
2000	Research Development Council, Worcester Polytechnic Institute. <i>Computational Algorithms for Analysis of Genomic Data</i> . \$19,000. <u>Principal Investigator</u> (with S. Alvarez, C. Ruiz, L. Ryder, and M. Stevens).
1999	<i>Travel Award to attend the 3rd Gordon Research Conference in Molecular Evolution in Hayama, Japan</i> . Gordon Research Conferences and the National Science Foundation.
1997-1998	Minnie L. Maffett Fellowship Fund. Texas Federation of Business and Professional Women's Clubs, Inc. <i>Minnie L. Maffett Fellowship</i> .
1995	Graduate School of Biomedical Sciences. The University of Texas-Houston. <i>Student Travel Award</i> .
1988-1990	Novosibirsk State University, Russia. <i>Scholarship for academic excellence and scientific achievements</i>
1988	Novosibirsk State University, Russia. <i>Scientific Council Scholarship</i> (for academic excellence).

Grant Reviewer

2011	Ad hoc reviewer for a National Institutes of Health special emphasis panel, ZRG1 PSE-K 03M, Member Conflict: Epidemiology.
2002 – 2003	U.S. National Science Foundation Advisory Panel member
<i>Mail reviewer:</i>	
2000-2009	U.S. National Science Foundation
2008	Thomas F. and Kate Miller Jeffress Memorial Trust
1997-1999	U.S. Civilian Research and Development Foundation

Reviewer for Scientific Journals

Circulation	Proceedings of the National Academy of Sciences USA
OMICS	Genetic Epidemiology
Molecular Biology and Evolution	BioSystems
Hypertension	Molecular Phylogenetics and Evolution
Bioinformatics	Journal of Molecular Evolution
Journal of Biomolecular Structure and Dynamics	Functional and Integrative Genomics
Database	Journal of Proteomics
African Journal of Biotechnology	Chemistry and Biodiversity

Invited Seminar, Colloquium, and Conference Speaker

- 08/2014 *Computational analysis of genome, expression, and epigenetic information in human and model bacteria.* Biometric Research Branch, Division of Cancer Treatment and Diagnosis, National Cancer Institute, NIH, Rockville, MD
- 10/2011 *Linking genome variation to phenotypic outcomes: Genetic, epigenetic, and transcriptomic analysis of longitudinal cohort data.* Center for Scientific Review, National Institutes of Health, Bethesda, MD
- 03/2011 *Linking genome variation to phenotypic outcomes: Genetic and epigenetic analysis of a longitudinal cohort.* Program in Bioinformatics, University of Memphis, Memphis, TN
- 03/2010 *Bioinformatics analysis of genome, sequence, and gene expression information: applications to bacterial, viral, and human data.* Department of Biology, Murray State University, Murray, KY
- 04/2009 *Phylogenetic analyses of genome sequence information from bacteria, viral pathogens, and human immune defense components.* Program in Bioinformatics, University of Memphis, Memphis, TN
- 03/2009 *Bioinformatic analysis of genome, sequence, and expression information: an application to bacterial data. Distinguished alumna presentation.* 13th Annual Symposium, Human and Molecular Genetics Program. Graduate School of Biomedical Science, The University of Texas Health Science Center at Houston
- 12/2008 *Bioinformatics analysis of genome, sequence, and expression information.* Department of Medical Genetics, Cedars Sinai Medical Center, Los Angeles, CA
- 10/2008 *Bioinformatic analysis of bacterial gene regulation and of human and viral complement regulators.* Center for the Study of Biological Complexity, Virginia Commonwealth University. Richmond, VA
- 05/2008 IEEE 2008 International Conference on BioMedical Engineering and Informatics (BMEI 2008). Sanya, China. **Invited platform presenter:** J. Krushkal, M. Puljic, B. Yan, J. F. Barbe, R. Mahadevan, B. Postier, R. A. O'Neil, G. Reguera, C. Leang, L. N. DiDonato, C. Núñez, B. A. Methé, R. M. Adkins, and D. R. Lovley. *Genome regions involved in multiple regulatory pathways identified using GSEL, a genome-wide database of regulatory sequence elements of Geobacter sulfurreducens*
Session Chair: "Applications of artificial intelligence in bioinformatics and medical informatics III"
- 11/2007 *Bioinformatic analysis of transcriptional regulation of environmentally important bacterial species.* Science Series (joint program between Departments of Biological Sciences and of Chemistry and Physics). Arkansas State University. Jonesboro, AR
- 09/2007 *Bioinformatic analysis of transcriptional regulatory sites.* Program in Bioinformatics, University of Memphis, Memphis, TN
- 07/2007 *Bioinformatic analysis of bacterial, viral, and human genome data.* School of Biological Sciences, University of Sydney, Australia
- 10/2005 *Bioinformatics analysis of sequence, genome and expression information.* Department of Computer Science, University of Memphis, Memphis, TN
- 06/2005 *Bioinformatics analysis of genome and expression information: applications to bacterial, viral, and human data.* Department of Sciences, Holon Academic Institute of Technology, Tel Aviv, Israel
- 12/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, University of Memphis. Memphis, TN
- 05/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, Virginia State University. Colonial Heights, VA

- 05/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biological Sciences, California State University at Pomona. Pomona, CA
- 04/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biological Sciences, University of the Sciences in Philadelphia. Philadelphia, PA
- 03/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, University of Kentucky. Lexington, KY
- 02/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, St. Edward's University. Austin, TX
- 02/2004 *Computational analysis of bacterial, viral, and human genome data.* Department of Biology, Texas A&M University. College Station, TX
- 04/2003 *Computational analysis of genetic data: bacteria, viruses, and human.* Department of Zoology, Oklahoma State University. Stillwater, OK
- 06/2001 *Computational analysis of biological information at sequence and genome level.* Department of Medicine, The University of Texas Health Science Center at San Antonio. San Antonio, TX
- 06/2001 *Computational analysis of biological information at sequence and genome level.* The University of Tennessee Health Science Center. Memphis, TN
- 03/2001 *Computational analysis of DNA and protein sequences.* Department of Biology, Amherst College. Amherst, MA. Presentation for undergraduate students.
- 01/2001 *Computational genomic analysis of human immunity and pathogenic organisms.* Department of Microbiology, University of Massachusetts. Amherst, MA.
- 11/1999 *Computational analysis of DNA data at sequence and genome level.* Program in Molecular and Cellular Biology, Department of Biochemistry and Molecular Biology, University of Massachusetts. Amherst, MA
- 02/1999 *Computational analysis of DNA data at sequence and genome level.* Department of Biology and Biotechnology. Worcester Polytechnic Institute. Worcester, MA
- 02/1998 *Multipoint gene mapping for essential hypertension. Invited Alumna Presentation.* The 5th Annual Genetics Mini-Symposium. Graduate School of Biomedical Science, The University of Texas-Houston Health Science Center.
- 11/1997 *Use of multipoint methods for gene mapping of essential hypertension.* W.M. Keck Center for Computational Biology, Rice University. Houston, TX
- 09/1997 *Molecular evolution of primate RNA viruses.* Department of Ecology and Evolutionary Biology, Rice University. Houston, TX
- 02/1997 *Computational analysis of DNA data at sequence and genome levels.* Institute of Molecular Medicine, The University of Texas Health Science Center. Houston, TX
- 10/1995 *Phylogenetic tree reconstruction for primate immunodeficiency viruses.* Colloquium. Department of Statistics, Rice University. Houston, TX
- 03/1992 *Role of CpG dinucleotides in evolution of Alu and B2 repeats in mammalian genomes.* Laboratory of Cryptobiology, Department of Polymer Research, Weizmann Institute of Science. Rehovot, Israel
- 03/1992 *Possible scheme of evolution of interspersed repeats in mammalian genomes.* Department of Mathematics and Computer Science, Bar-Ilan University. Ramat Gan, Israel

Seminar presentations for inter-institutional working groups and projects

- 04/2011 *GWAS and other bioinformatic analyses in CANDLE.* Nutrigenomics conference organized by the CANDLE (Conditions Affecting Neurocognitive Development and Learning in Early Childhood) Project, the Urban Child Institute, and The University of Tennessee Health Science Center. Memphis, TN.
- 04/2010 *An update on genetic and epigenetic analysis in the CANDLE Project.* Conditions Affecting Neurocognitive Development and Learning in Early Childhood (CANDLE) project meeting, Memphis, TN.
- 09/2009 *An update on computational analysis of molecular evolution and transcriptional regulation of Geobacteraceae.* 5th Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 10/2008 *Computational Analysis of Transcriptional Regulation in Geobacteraceae.* 4th Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 10/2007 *Bioinformatic Analysis of Transcriptional Regulation in Geobacteraceae.* 3rd Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 07/2007 *Bioinformatic data analysis.* Bioinformatics and Biodiversity Laboratory (Dr. Lars Jermiin, Head), University of Sydney, Australia
- 10/2006 *Computational analysis of transcriptional regulation in Geobacteraceae.* 2nd Annual Genomics:GTL Geobacter Project meeting, University of Massachusetts, Amherst, MA
- 06/2006 *Computational analysis of transcriptional regulation: an update.* Geobacter group, Department of Microbiology, University of Massachusetts, Amherst, MA
- 10/2005 *Computational prediction of operons and transcriptional regulation.* 1st Annual Genomics:GTL Geobacter Project Meeting, University of Massachusetts, Amherst, MA
- 09/2003 *Computational prediction of operons and transcription factor binding sites in Geobacteraceae: an update.* Geobacter group, University of Massachusetts, Amherst, MA
- 03/2003 *Prediction of transcription factor binding sites in Geobacteraceae.* Geobacter group, Department of Microbiology, University of Massachusetts, Amherst, MA
- 05/1998 *Results of the genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Rio Grande City, TX
- 04/1997 *Genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Houston, TX
- 11/1997 *Update on the genome-wide scan for hypertension-related genes.* Genetic Analysis of Atherosclerosis steering committee meeting. Jackson, MS
- 10/1996 *Linkage mapping of hypertension-related genes.* Blood Pressure Linkage Working Meeting. Department of Human Genetics, University of Michigan. Ann Arbor, MI

Grant Review Outreach

- 03.20.2014 Led round table discussions of NIH grant review for early career investigators at the American Heart Association Epidemiology and Prevention, and Nutrition, Physical Activity and Metabolism 2014 Scientific Sessions, AHA EPI/NPAM 2014 (with NHLBI program staff).
- 01.08.2014 2014 New Grantee Workshop of the National Cancer Institute Division of Cancer Control and Population Genetics. Presentation: Review process and grant renewal.
- 04.20.2013 Conducted a mock study section review meeting at the Young Investigator Forum of the American Academy of Sleep Medicine (jointly with NHLBI staff).

Conference organizer and/or session chair

- 03/2012 11th annual UT-ORNL-KBRIN Bioinformatics Summit. Louisville, KY.
Planning committee member
- 06/2011 The 2011 Summit on Systems Biology - Molecular Networks and Disease. Richmond, VA
Program committee member.
- 04/2011 CANDLE Nutrigenomics conference. Organized by The Urban Child Institute and the University of Tennessee Health Science Center. Memphis, TN.
Planning committee member
- 04/2011 10th annual UT-ORNL-KBRIN Bioinformatics Summit 2011. Memphis, TN.
Planning committee member
- 03/2010 UT-ORNL-KBRIN Bioinformatics Summit 2010. Lake Barkley State Park, Cadiz, KY.
Planning committee member
- 06/2009 The Third Summit on Systems Biology – The Microbial World and Beyond. Richmond, VA
Program committee member
- 03/2009 UT-ORNL-KBRIN Bioinformatics Summit 2009. Falls Creek Falls State Park, Pikeville, TN
Planning committee member. Session Chair: “Systems Biology”
- 05/2008 IEEE 2008 International Conference on BioMedical Engineering and Informatics (BMEI 2008). Sanya, China.
Session Chair: “Applications of artificial intelligence in bioinformatics and medical informatics III”
- 03/2008 UT-ORNL-KBRIN Bioinformatics Summit 2008. Lake Barkley State Park, Cadiz, KY.
Planning committee member.
- 08/1990 Modeling and Computer Methods in Molecular Biology and Genetics (International Conference). Novosibirsk, Russia. ***Member of the organizing committee.***

Scientific Review Administration (01.2012-10.2014)

Organized NIH Center for Scientific Review meetings to review applications in the areas of epidemiology, genetics, and epigenetics of cardiovascular outcomes, sleep, cancer, lung, blood, neuromuscular, and skeletal disorders, aging, and early child development.

Teaching Experience

2009-2011	BIOE 824 <i>Genetic Epidemiology</i> . Department of Preventive Medicine/M.S. Program in Epidemiology, University of Tennessee Health Science Center
2008-2010	Guest lecturer in a graduate course, MSCI815 <i>Bioinformatics II</i> (HapMap Project module)
2007-2011	Guest lecturer in a graduate course, BINF 7980, <i>Seminar in Bioinformatics</i> . Graduate Program in Bioinformatics, University of Memphis
2003-2009	BIOE 825 <i>Bioinformatics for Epidemiologists</i> . Department of Preventive Medicine/M.S. Program in Epidemiology, University of Tennessee Health Science Center
2008	Educational seminars for the University of Tennessee-Memphis faculty and staff: <i>Recent advances in genomics, microarray technology, and proteomics, and their application to human health</i> <i>The International HapMap Project: a rich resource of genetic information</i>
2005-2008	Guest lecturer in a graduate course, BIOE 824 <i>Genetic Epidemiology</i> . Department of Preventive Medicine/Program in Epidemiology, University of Tennessee Health Science Center (lectures on microarray analysis)
2007	Guest lecturer in a graduate course, BIOE 840 <i>Special Topics: Applications from the Basic Sciences</i> . Department of Preventive Medicine/Program in Epidemiology, University of Tennessee Health Science Center (lectures on microarray analysis)
2004	Guest lecturer in a junior level course, <i>Cellular and Molecular Biology</i> . St. Edward's University, Austin, TX
2004	Teaching seminar in bioinformatics, <i>Sequence Alignments</i> . Virginia State University, Colonial Heights, VA
2002	<i>Bioinformatics for Epidemiologists</i> (seminar for faculty and staff). Department of Preventive Medicine and Center of Genomics and Bioinformatics, University of Tennessee-Memphis
2000-2002	BB4440 and BB544 <i>Bioinformatics</i> (for seniors and graduate students). Department of Biology and Biotechnology, Worcester Polytechnic Institute. BB3512 <i>Molecular Genetics</i> - a computational biology techniques course (for juniors). BB501 <i>Graduate Student Seminar and Invited Research Seminar</i>
1999	Participant in a Bioinformatics College Teachers Workshop. Boston University, Program in Bioinformatics. Guest lecturer in an undergraduate course: <i>Molecular Evolution</i> . University of Massachusetts, Amherst
1996-1998	Guest lecturer in graduate courses (The University of Texas-Houston Health Science Center): <i>Computational Sequence Analysis</i> <i>Genetics of Human Disease</i> <i>Biochemistry</i>

Publications

Manuscripts and Book Chapters (Peer reviewed)

1. **J. Krushkal**, L. E. Murphy, F. B. Palmer, J. C. Graff, C. A. Hovinga, K. Mozhui, F. Thomas, V. Park, T. R. Sutter, F. A. Tylavsky, and R. M. Adkins (2014) *Epigenetic analysis of neurocognitive development at 1 year of age in a community-based pregnancy cohort*. Behavior Genetics, 44(2):113-125
2. R. M. Adkins, F. A. Tylavsky, and **J. Krushkal** (2012) *Newborn umbilical cord blood DNA methylation and gene expression levels exhibit limited association with birth weight*. Chemistry and Biodiversity, 9(5):888-899.
3. **J. Krushkal**, Y. Qu, D. R. Lovley, and R. M. Adkins (2012) *Phylogenetic classification of diverse LysR-type transcriptional regulators of a model prokaryote Geobacter sulfurreducens*. Journal of Molecular Evolution. 74(3-4):187-205
4. R. M. Kelsey, B. S. Alpert, M. K. Dahmer, **J. Krushkal**, and M. W. Quasney (2011) *Alpha-adrenergic receptor polymorphisms and cardiovascular reactivity to stress in Black adolescents and young adults*. Psychopharmacology. 49(3):401-412.
5. J. W. Schroeder, K. N. Conneely, J. C. Cubells, V. Kilaru, D. J. Newport, B. T. Knight, Z. N. Stowe, P. A. Brennan, **J. Krushkal**, F. A. Tylavsky, R. N. Taylor, R. M. Adkins, A. K. Smith (2011) *Neonatal DNA methylation patterns associate with gestational age*. Epigenetics 6(12), 1498-1504.
6. R. M. Adkins, F. Thomas, F. A. Tylavsky, and **J. Krushkal** (2011) *Parental ages and levels of DNA methylation in the newborn are correlated*. BMC Medical Genetics 12:47. **Highly accessed article**.
7. **J. Krushkal**, S. Sontineni**, C. Leang, Y. Qu, R. M. Adkins, D. R. Lovley (2011) *Genome diversity of the TetR family of transcriptional regulators in a metal-reducing family bacterial Geobacteraceae and other microbial species*. OMICS: A Journal of Integrative Biology, 15(7-8):495-506.
8. R. M. Adkins, **J. Krushkal**, F. A. Tylavsky, F. Thomas (2011) *Racial differences in gene-specific DNA methylation levels are present at birth*. Birth Defects Research (Part A). 91:728-736
9. **J. Krushkal**, K. Juarez, J. F. Barbe, Y. Qu, A. Andrade, M. Puljic, R. M. Adkins, D. R. Lovley, and T. Ueki. *Genome-wide survey for PilR recognition sites of a metal-reducing prokaryote Geobacter sulfurreducens* (2010) Gene 469:31-44.
10. R. M. Adkins, G. Somes, J. C. Morrison, J. B. Hill, E. W. Watson, E. F. Magann, and **J. Krushkal**. *Association of Birth Size with Polymorphisms in the IGF2, H19 and IGF2R Genes* (2010) Pediatric Research 68: 429-434.
11. R. M. Kelsey, B. S. Alpert, M. K. Dahmer, **J. Krushkal**, and M. W. Quasney. *Beta-adrenergic receptor polymorphisms and cardiovascular reactivity to stress in black adolescents and young adults* (2010) Psychophysiology, 47:863-73.
12. R. M. Adkins, **J. Krushkal**, F. Tylavsky, E. F. Magann, C. K. Klauser, J. C. Morrison, and G. Somes (2010) *Association of maternally inherited GNAS alleles with African-American male birth weight*. International Journal of Pediatric Obesity 5: 177-184
13. P. K. Fung, **J. Krushkal**, and P. Weathers. *Computational analysis of the evolution of 1-deoxy-D-xylulose-5-phosphate reductoisomerase in plants* (2010) Chemistry and Biodiversity 7:1098-1110
14. Y. Qu, P. Brown, J. F. Barbe, M. Puljic, E. Merino, R. M. Adkins, D. R. Lovley, and **J. Krushkal** (2009) *GSEL v. 2, a genome-wide query system of operon organization and regulatory sequence elements of Geobacter sulfurreducens*. OMICS 13: 439-449
15. C. Leang, **J. Krushkal**, T. Ueki, M. Puljic, K. Juárez, C. Núñez, G. Reguera, R. DiDonato, B. Postier, R. M. Adkins, and D. R. Lovley, *RpoN is an essential sigma factor in Geobacter sulfurreducens* [**Equal first author contributor**]. (2009) BMC Genomics 10: 331
16. M. Aklujkar, **J. Krushkal**, G. DiBartolo, A. Lapidus, M. L. Land, and D. R. Lovley (2009) *The genome sequence of Geobacter metallireducens: features of metabolism, physiology and regulation common and dissimilar to Geobacter sulfurreducens*. BMC Microbiology 9:109. **Highly accessed article**.
17. **J. Krushkal**, C. Leang, Y. Qu, B. Yan, J. F. Barbe, M. Puljic, R. M. Adkins, and D. R. Lovley (2009) *Diversity of promoter elements in the upstream regions of differentially expressed operons of a Geobacter sulfurreducens mutant adapted to disruption in electron transfer*. Functional and Integrative Genomics 9:15-25
18. P. Patwari, P. A. O'Cain, D. M. Goodman, M. E. Smith, **J. Krushkal**, G. Somes, C. Liu, M. W. Quasney, M. Dahmer (2008) *Interleukin-1 receptor antagonist intron 2 polymorphism and respiratory failure in children with community-acquired pneumonia*. Pediatric Critical Care Medicine 9:1-7.

19. H. T. Tran, **J. Krushkal**, F. Antomatei, R. H. Glaven, D. R. Lovley, and R. M. Weis (2008) *Comparative genomics of Geobacter chemotaxis genes reveals a diversity of signaling functions*. BMC Genomics 9:471
20. **J. Krushkal**, M. Puljic, B. Yan, J. F. Barbe, R. Mahadevan, B. Postier, R. A. O'Neil, G. Reguera, C. Leang, L. N. DiDonato, C. Núñez, B. A. Methé, R. M. Adkins, and D. R. Lovley (2008) *Genome regions involved in multiple regulatory pathways identified using GSEL, a genome-wide database of regulatory sequence elements of Geobacter sulfurreducens*. In: BMEI2008. Biomedical engineering and informatics: new developments and the future. Proceedings the First International Conference on Biomedical Engineering and Informatics. Y. Peng and Y. Zhang (Eds). Vol. 1, pp. 424-431. IEEE Computer Society, Las Alamitos, CA
21. R. Mahadevan, B. Yan, B. Postier, K. Nevin, R. O'Neil**, M. Coppi, B. Methé, and **J. Krushkal** (2008) *Characterizing regulation of metabolism in Geobacter sulfurreducens through genome-wide expression data and sequence analysis*. OMICS 12:1-27
22. R. M. Adkins, **J. Krushkal**, C. K. Klauser, J. F. Magann, J. C. Morrison, and G. A. Somes (2008). *Association between small for gestational age and paternally inherited 5' insulin haplotypes*. International Journal of Obesity 32:372-380
23. R. M. Adkins, C. K. Klauser, E. F. Magann, **J. Krushkal**, T. K. Boyd, J. N. Fain, and J. C. Morrison (2007) *Site -2,548 of the leptin gene is associated with gender-specific trends in newborn size and cord leptin levels*. International Journal of Pediatric Obesity 16: 1-8
24. V. M. Park, B. C. Mason, R. Li, **J. Krushkal**, C. Riely, and J. Fleckenstein (2007) *Racial differences in the hepatitis C quasiespecies: Association of reduced selection pressure with treatment failure*. Digestive Diseases and Sciences 52: 2540-2459
25. R. M. Adkins, J. Fain, **J. Krushkal**, C. K. Klauser, J. F. Magann, and J. C. Morrison (2007). *Association between paternally inherited haplotypes upstream of the insulin gene and umbilical cord IGF2 levels*. Pediatric Research 62:1-3
26. B. Yan, D. R. Lovley, and **J. Krushkal** (2007) *Genome-wide similarity search for transcription factors and their binding sites in a metal-reducing prokaryote Geobacter sulfurreducens*. BioSystems 90: 421-444
27. **J. Krushkal**, B. Yan, L. N. DiDonato, M. Puljic, K. P. Nevin, T. L. Woodard, R. M. Adkins, B. A. Methé, and D. R. Lovley (2007) *Genome-wide expression profiling in Geobacter sulfurreducens: Identification of Fur and RpoS transcription regulatory sites using a rel_{Gsu} mutant*. Functional and Integrative Genomics 7:229-255
28. B. Yan, C. Núñez, T. Ueki, A. Esteve-Núñez, M. Puljic, R. M. Adkins, B. A. Methé, D. R. Lovley, and **J. Krushkal** (2006) *Computational prediction of RpoS and RpoD regulatory sites in Geobacter sulfurreducens using sequence and gene expression information*. Gene 384:73-95
29. E. Ciulla, A. Emery, D. Konz, and **J. Krushkal** (2005) *Computational sequence analysis of orthopoxvirus proteins similar to human complement regulators*. Gene 355:40-47
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